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RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/730,034

TIME: 14:25:50

Input Set : N:\Crif3\RULE60\10730034.raw

Output Set: N:\CRF4\08272004\J730034.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Takanori OKURA
 6 Kakuji TORIGOE
 7 Masahi KURIMOTO

9 (ii) TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
 10 OF INDUCING THE PRODUCTION OF INTERFERON-

12 (iii) NUMBER OF SEQUENCES: 35

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: BROWDY AND NEIMARK
 16 (B) STREET: 419 Seventh Street, N.W., Suite 300
 17 (C) CITY: Washington
 18 (D) STATE: D.C.
 19 (E) COUNTRY: USA
 20 (F) ZIP: 20004

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: Patent In Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/730,034
 C--> 30 (B) FILING DATE: 09-Dec-2003
 31 (C) CLASSIFICATION: 435

33 (vii) PRIOR APPLICATION DATA:

W--> 34 (A) APPLICATION NUMBER: US/08/884,324
 35 (B) FILING DATE: 27-JUN-1997
 W--> 36 (A) APPLICATION NUMBER: JP 185,305/96
 37 (B) FILING DATE: 27-JUN-1996

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: BROWDY, Roger L.
 41 (B) REGISTRATION NUMBER: 25,618
 42 (C) REFERENCE/DOCKET NUMBER: OKURA=1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 202-628-5197
 46 (B) TELEFAX: 202-737-3528

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 157 amino acids
 52 (B) TYPE: amino acid
 53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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```

59 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
60 1 5 10 15
61 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
62 20 25 30
63 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
64 35 40 45
65 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
66 50 55 60
W--> 67 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
68 65 70 75 80
69 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
70 85 90 95
71 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
72 100 105 110
73 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
74 115 120 125
75 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
76 130 135 140
77 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
78 145 150 155
80 (2) INFORMATION FOR SEQ ID NO: 2:
82 (i) SEQUENCE CHARACTERISTICS:
83 (A) LENGTH: 1120 base pairs
84 (B) TYPE: nucleic acid
85 (C) STRANDEDNESS: double
86 (D) TOPOLOGY: linear
88 (ii) MOLECULE TYPE: cDNA to mRNA
90 (iii) HYPOTHETICAL: No
92 (iv) ANTI-SENSE: No
94 (vi) ORIGINAL SOURCE:
95 (A) ORGANISM: human
96 (F) TISSUE TYPE: liver
C--> 98 (ix) FEATURE:
102 (A) NAME/KEY: leader peptide
100 (B) LOCATION: 1..177
101 (C) IDENTIFICATION METHOD: E
112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
114 GCCTGGACAG TCAGCAAGGA ATGTGTCTCCC AGTGCAATTTT GCCCTCCTGG CTGCCAACTC 60
115 TGGCTGCTAA AGCGGCTGCC ACCTGCTGCA GTCTACACAG CTTCGGAAG AGGAAAGGAA 120
116 CCTCAGACCT TCCAGATCGC TTCCTCTCGC AACAAACTAT TTGTCGCAGG AATAAAG 177
117 ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG GCA ATG 225
118 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
119 -35 -30 -25
120 AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA GCT GAA GAT GAT GAA AAC 273
121 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
122 -20 -15 -10 -5
123 CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA GTC ATA 321
124 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
125 1 5 10

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```

126 AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT CGG CCT 369
127 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
128      15      20      25
129 CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA GAT AAT GCA CCC CGG 417
130 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
131      30      35      40
132 ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC CAG CCT AGA GGT ATG 465
133 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
134 45      50      55      60
135 GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT TCA AYT CTC TCC TGT 513
W--> 136 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
137      65      70      75
138 GAG AAC AAA ATT ATT TCC TTT AAG GAA ATG AAT CCT CCT GAT AAC ATC 561
139 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
140      80      85      90
141 AAG GAT ACA AAA AGT GAC ATC ATA TTC TTT CAG AGA AGT GTC CCA GGA 609
142 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
143      95      100      105
146 CAT GAT AAT AAG ATG CAA TTT GAA TCT TCA TCA TAC GAA GGA TAC TTT 657
147 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
148      110      115      120
149 CTA GCT TGT GAA AAA GAG AGA GAC CTT TTT AAA CTC ATT TTG AAA AAA 705
150 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
151 125      130      135      140
152 GAG GAT GAA TTG GGG GAT AGA TCT ATA ATG TTC ACT GTT CAA AAC GAA 753
153 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
154      145      150      155
155 GAC TAGCTATTAA AATTTTCATGC CGGGCGCAGT GGCTCACGCC TGTAATCCCA 806
156 Asp
157 GCCCTTTGGG AGGCTGAGGC GGGCAGATCA CCAGAGGTCA GGTGTTCAAG ACCAGCCTGA 866
158 CCAACATGGT GAAACCTCAT CTCTACTAAA AATACTAAAA ATTAGCTGAG TGTAGTGACG 926
159 CATGCCCTCA ATCCCAGCTA CTCAAGAGGC TGAGGCAGGA GAATCACTTG CACTCCGGAG 986
160 GTAGAGGTTG TGGTGAGCCG AGATTGCACC ATTGCGCTCT AGCCTGGGCA ACAACAGCAA 1046
161 AACTCCATCT CAAAAAATAA AATAAATAA TAAACAAATA AAAAATTCAT AATGTGAAAA 1106
162 AAAAAAAAAA AAAA 1120

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164 (2) INFORMATION FOR SEQ ID NO: 3:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 135 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: double

170 (D) TOPOLOGY: linear

172 (ii) MOLECULE TYPE: Genomic DNA

174 (vi) ORIGINAL SOURCE:

175 (A) ORGANISM: human

176 (F) TISSUE TYPE: placenta

C--> 178 (ix) FEATURE:

179 (A) NAME/KEY: exon

180 (B) LOCATION: 1..135

181 (C) IDENTIFICATION METHOD: S

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183      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
185  AA AAC CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA      47
186  Glu Asn Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser
187      -5              1              5              10
188  GTC ATA AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT      95
189  Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn
190      15              20              25
191  CGG CCT CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA G      135
192  Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp
193      30              35              40
195  (2) INFORMATION FOR SEQ ID NO: 4:
197      (i) SEQUENCE CHARACTERISTICS:
198          (A) LENGTH: 134 base pairs
199          (B) TYPE: nucleic acid
200          (C) STRANDEDNESS: double
201          (D) TOPOLOGY: linear
203      (ii) MOLECULE TYPE: Genomic DNA
205      (vi) ORIGINAL SOURCE:
206          (A) ORGANISM: human
207          (F) TISSUE TYPE: placenta
C--> 209      (ix) FEATURE:
210          (A) NAME/KEY: exon
211          (B) LOCATION: 1..134
212          (C) IDENTIFICATION METHOD: S
215      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
217  AT AAT GCA CCC CGG ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC      47
218  Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser
W--> 219  40              45              50              55
220  CAG CCT AGA GGT ATG GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT      95
221  Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile
W--> 222      60              65              70
223  TCA ACT CTC TCC TGT GAG AAC AAA ATT ATT TCC TTT AAG      134
224  Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys
W--> 225      80              85
227  (2) INFORMATION FOR SEQ ID NO: 5:
229      (i) SEQUENCE CHARACTERISTICS:
230          (A) LENGTH: 87 base pairs
231          (B) TYPE: nucleic acid
232          (C) STRANDEDNESS: double
233          (D) TOPOLOGY: linear
235      (ii) MOLECULE TYPE: Genomic DNA
237      (vi) ORIGINAL SOURCE:
238          (A) ORGANISM: human
239          (F) TISSUE TYPE: placenta
C--> 241      (ix) FEATURE:
242          (A) NAME/KEY: exon
243          (B) LOCATION: 1..87
244          (C) IDENTIFICATION METHOD: S
246      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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```

248 GAATAAAG ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG      50
249      Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val
250      -35                      -30                      -25
251 GCA ATG AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA G                      87
252 Ala Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala
253      -20                      -15                      -10
255 (2) INFORMATION FOR SEQ ID NO: 6:
257     (i) SEQUENCE CHARACTERISTICS:
258         (A) LENGTH: 12 base pairs
259         (B) TYPE: nucleic acid
260         (C) STRANDEDNESS: double
261         (D) TOPOLOGY: linear
263     (ii) MOLECULE TYPE: Genomic DNA
265     (vi) ORIGINAL SOURCE:
266         (A) ORGANISM: human
267         (F) TISSUE TYPE: placenta
C--> 269     (ix) FEATURE:
270         (A) NAME/KEY: exon
271         (B) LOCATION: 1..87
272         (C) IDENTIFICATION METHOD: S
274     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
276 CT GAA GAT GAT G                      12
277 Ala Glu Asp Asp Glu
278 -10
280 (2) INFORMATION FOR SEQ ID NO: 7:
282     (i) SEQUENCE CHARACTERISTICS:
283         (A) LENGTH: 2167 base pairs
284         (B) TYPE: nucleic acid
285         (C) STRANDEDNESS: double
286         (D) TOPOLOGY: linear
288     (ii) MOLECULE TYPE: Genomic DNA
290     (vi) ORIGINAL SOURCE:
291         (A) ORGANISM: human
292         (F) TISSUE TYPE: placenta
C--> 294     (ix) FEATURE:
295         (A) NAME/KEY: exon + 3'UTR
296         (B) LOCATION: 1..2167
297         (C) IDENTIFICATION METHOD: E
299     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
301 GAA ATG AAT CCT CCT GAT AAC ATC AAG GAT ACA AAA AGT GAC ATC ATA      48
302 Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys Ser Asp Ile Ile
W--> 303 85                      90                      95                      100
304 TTC TTT CAG AGA AGT GTC CCA GGA CAT GAT AAT AAG ATG CAA TTT GAA      96
305 Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys Met Gln Phe Glu
W--> 306                      105                      110                      115
307 TCT TCA TCA TAC GAA GGA TAC TTT CTA GCT TGT GAA AAA GAG AGA GAC      144
308 Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp
W--> 309                      120                      125                      130
310 CTT TTT AAA CTC ATT TTG AAA AAA GAG GAT GAA TTG GGG GAT AGA TCT      192

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/27/2004
PATENT APPLICATION: US/10/730,034 TIME: 14:25:51

Input Set : N:\Crif3\RULE60\10730034.raw
Output Set: N:\CRF4\08272004\J730034.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.73

Seq#:2; Xaa Pos.73

VERIFICATION SUMMARY

DATE: 08/27/2004

PATENT APPLICATION: US/10/730,034

TIME: 14:25:51

Input Set : N:\Crf3\RULE60\10730034.raw

Output Set: N:\CRF4\08272004\J730034.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:64
L:98 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:102 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:105 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:108 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:513
L:178 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:209 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:241 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:269 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:294 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:364 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:409 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:511 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:681 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:726 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:805 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:809 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:812 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:815 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:818 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:821 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:824 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:827 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:830 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:833 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:836 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:839 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:874 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:933 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:934 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:940 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:943 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:966 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:967 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10730034.raw

Output Set: N:\CRF4\08272004\J730034.raw

L:970 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:976 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1056 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1059 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1087 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1091 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1094 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1097 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1100 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1103 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1106 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1109 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1112 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1115 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1118 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1121 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2) (ix)
L:1417 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1476 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1509 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1599 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1602 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1605 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1608 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1611 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14